

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 14, 2003, 11:42:22 ; Search time 7317.37 seconds

11470.644 million cell updates/sec

Title: US-05-910-428-1

Sequence: 1 ctctgaagatccttctttcagtg...aatcaaggaattllagacgctc 2863

Scoring table: IDENTITY_NUC

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Maximum seq length: 0

Post-processing: Minimum Match 0%

Maximum Match 1000
Listing first 45 s

Database : GenEmbl : ♦

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GenEmb1: *
1: qb_ba: *
2: 3h_b'a *
3: qb_in: *
4: qb_cm: *
5: qb_ov: *
6: qb_pat: *
7: qb_ph: *
8: qb_pl: *
9: qb_pr: *
10: qb_ro: *
11: qb_sts: *
12: qb_sy: *
13: qb_un: *
14: qb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_cm: *
21: em_or: *
22: cm_ov: *
23: cm_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: cm_sts: *
28: em_un: *
29: em_vl: *
30: em_hlg_hum: *
31: em_hlg_inv: *
32: em_hlg_other: *
33: em_hlg_mus: *
34: em_hlg_pln: *
35: em_hlg_rod: *
36: em_hlg_mam: *
37: em_hlg_vrt: *
38: em_sy: *
39: em_hlgo_hum: *
40: em_hlgo_mus: *
41: em_hlgo_other: *

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB	ID	Description
1	2817	98.2	25688	4	BNU15731	U15731 Hos taurus
2	1128.6	39.1	174419	2	AC119060	AC119060 Hos tauru
3	1128.6	39.3	208327	2	AC119061	AC119061 Hos tauru
4	1112.8	38.6	149984	2	AC109789	AC109789 Hos tauru
5	1107.8	38.6	135794	2	AC109792	AC109792 Hos tauru
6	1105	38.6	144500	2	AC109790	AC109790 Hos tauru
7	1104.4	38.5	167368	2	AC109799	AC109799 Hos tauru
8	1096.2	38.2	154598	2	AC109787	AC109787 Hos tauru
9	1089.2	38.0	174419	2	AC119060	AC119060 Hos tauru
10	1077.4	37.5	178026	2	AC109914	AC109914 Bos tauru
11	1076	37.5	190076	2	AC108895	AC108895 Bos tauru
12	1075.4	37.5	205140	2	AC109793	AC109793 Bos tauru
13	1069	37.3	151482	4	AA453325	AA453325 Bos tauru
14	1062.8	37.0	183383	4	AC091252	AC091252 Hos tauru
15	1059.2	36.9	166277	2	AC109794	AC109794 Hos tauru
16	1056.4	36.8	168497	2	AC107410	AC107410 Bos tauru
17	1053.2	36.7	186071	2	AC126330	AC126330 Bos tauru
18	1041.2	36.3	203696	4	AC087860	AC087860 Bos tauru
19	1040.6	36.3	154921	2	AC109793	AC109793 Hos tauru
20	1039.2	36.2	150594	2	AC108889	AC108889 Hos tauru
21	1033	36.0	157115	2	AC129070	AC129070 Hos tauru
22	1028.4	35.8	173407	2	AC108887	AC108887 Bos tauru
23	1026.4	35.8	156512	2	AC109792	AC109792 Bos tauru
24	1018.6	35.5	227410	2	AC108693	AC108693 Bos tauru
25	1011.8	35.3	165933	2	AC109797	AC109797 Hos tauru
26	1003.8	35.0	12955	4	B0V1189	B0V1189 Hos taurus
27	1003.4	35.0	134662	2	AC109786	AC109786 Hos tauru
28	1003.4	35.0	141089	2	AC109915	AC109915 Bos tauru
29	989	34.5	134652	2	AC109780	AC109780 Bos tauru
30	984	34.5	141084	2	AC109915	AC109915 Bos tauru
31	988.8	34.5	12039	4	BNU25610	BNU25610 Hos taurus
32	972.6	33.9	164582	4	AC098686	AC098686 Hos tauru
33	972.6	33.9	149756	4	AC098629	AC098629 Hos tauru
34	970.4	33.8	214404	2	AC109407	AC109407 Bos tauru
35	961.4	33.5	147942	4	AC108994	AC108994 Bos tauru
36	958.4	33.4	108538	2	AC108893	AC108893 Bos tauru
37	956.4	33.3	12232	4	B0V15020A	B0V15020A Hos taurus
38	945	32.9	163311	2	AC109788	AC109788 Hos tauru
39	943.2	32.9	175942	2	AC107065	AC107065 Hos tauru
40	943	32.9	10666	4	GM2925285	GM2925285 Gvis latip
41	921.4	32.2	108548	2	AC108933	AC108933 Bos tauru
42	921.5	32.1	233345	2	AC121481	AC121481 Bos tauru
43	916.4	31.9	166277	2	AC100994	AC100994 Hos tauru
44	914.4	31.9	188121	2	AC099394	AC099394 Hos tauru
45	914	31.9	196377	4	AC105306	AC105306 Hos tauru

ALIGNMENTS

RESULT 1	BTU15731	25668 bp	DNA	linear	MM 04-SEP-2001
LOCUS	BTU15731				
DEFINITION	Bos taurus somatotropin receptor gene, exon 1 and liver-specific promoter region.				
ACCESSION	U15731				
VERSION	U15731.2	GI:13570031			
KEYWORDS					
SOURCE					
ORGANISM	Bos taurus.				
	Bos taurus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.				
REFERENCE	1 (bases 1 to 25668)				
AUTHORS	Heap, D., Lucy, M.C., Collier, R.J., Boyd, C.K. and Warren, W.C.				

[illegible]

ACCESSION AC109790
VERSION AC109790.2 C1:21955008
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT
SOURCE Bos taurus,

REFERENCE	AUTHORS
1 (bases 1 to 188500)	Akhter, N., Antocellis, J.

Benjamin, B., Blakeley, R.W., Boulard, G.G., Blevins, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.T., Iddell, J., Karlins, E., Lalle, P., Lee, T.S.-C., Legaspi, R., Maduro, O.L., Maduro, V.B., Marquelles, E.H., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, T.C., McDowell, J., Pagnalliran, C., Pearson, R., Forlino M.P., Prasad A., Schiele, M.G., Staniforth, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurganov, C., Vogel, J.L., Walker, M.A., Wechter, K.D., Wiggins, L., Young, A., Zhang, C. and Green, E.D.

NISC Comparative Sequencing Initiative

JOURNAL
OF
BACTERIOLOGY

REFERENCE
2 (pages 1 to 168500)

JOURNAL. Submitted (07 FEB 2002) NIH Intramural Sequencing Center, 8717
Government Circle, Bethesda, MD 20877, USA
REFERENCE 3 (bases 1 to 188500)

JOURNAL. Submitted (25 JUL 2002) NIH Intramural Sequencing Center, 871
Grovermont Circle, Gaithersburg, MD 20877, USA
COMMENT. On Jul 25, 2002 this sequence version replaced gi:18581929.

Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: <http://www.nisc.nih.gov>
Contact: nisc_zoo@nigr.nih.gov

Project Information
Center project name: axl
Center clone name: 040N24

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated strand and orientation of each sequence contig has been established using one or more of the following: read-pair data (from individual subclones), overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies; the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

Sequencing vector: *Plasmid, n/a*, 100% of reads
Chemistry: Dye terminator Big Dye, 100% of reads
Assembly program: Phrap, version 0.990319
Consensus quality: 187613 bases at least 40
Consensus quality: 187647 bases at least 50
Consensus quality: 188010 bases at least 60
Insert size: 13500, average: fp
Insert size: 188100, sum of contigs
Quality coverage: 12.73x in Q20 bases
Quality coverage: 9.14x in Q20 bases, sum of contigs

NOTE: This is a "working draft" sequence. It currently consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces are believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.

This sequence will be replaced by the finished sequence as soon as it is available and

* The accession number will be preserved.

* 156410	contig of 156410 bp in length
* 156411	156510: gap of unknown length
* 156511	170593: contig of 14483 bp in length
* 170594	171093: gap of unknown length
* 171094	181495: contig of 10402 bp in length
* 181496	181595: gap of unknown length
* 181596	187318: gap of unknown length
* 187319	contig of 5723 bp in length
* 187410	187418: gap of unknown length
* 187411	188502: contig of 1062 bp in length.
	Location/Qualifiers

misc_feature 1.156410

misc_feature

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BASE COUNT	ORIGIN
58730	a
38877	c
37404	g
53089	t
400	others

Query Match	36.6%	Score 1106, len 4	length 198500
Best Local Similarity	92.8%	Pred. No. 6.7e-256	
Matches 1193; Conservative	0;	Mismatches 90;	Indels 3; Gaps 3

09 1029 AAGCTTTAAATTTTTTTTCTCCAAATTTATTTATTTTAAAGTTACATAATG 1088

QY 1389 TATTAGTTTGTCCAAATACAAAAGAAATCGGACAGGTATTACAGTGTCCCATACCG 1148

DB 13/20 1A11AG111GCCCCAATACAAAAGAACCCGCGACAGCA1ATAACATGT3471CCCATCT 13661

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Q7 1267 TATTATTTTATTGATTTCTAAATTTTTTAAGGTTCCTCCTCCACAGAGTCCA 1326

1327 TAAGATTGTTTATATATAGTGTCTT1155TGTCGTAAGAGGGGTAATGTAAC 1386

Db 13480 TAAAGCTGTTCTATACATCAGTGTCTCTTTGATGTCCTGATACAGGGGATTATTGTTACG 13421

Ub 13420 ATCTTCTAAATTCATATATATGCTTACATATACGTATTCATCTTTTCCTTCCTTCGCT 13361

NOTE: This is a working draft sequence. It currently consists of 18 fragments. The π value of the fragment is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

Location: 154998

```

/NOTE="assembly_fragment
clone_end:"7
vector_side:left"

```

```

/001 e- "assembly_fragment
66404. .154938
/001 e- "assembly_fragment

```

HASPE COUNT	45594	d	32581	e	32935	f	43688	g	200 others
ORIGIN									

Query Match	38.28;	Score	1096.2;	DB 2;	Length	154998;
Host Label Similarity	97.08;	Pred. No.	1.50	253;		
Matches 1149;	Conservative	0;	Mismatches	34;	Indels	3;
					Gaps	3

[illegible][illegible]

Benjamin, B., Blakesley, R. W., Hoffart, J. S., Street, K., Hinkley, C., Brooks, S., Dietrich, H. L., Grallic, S., Gali, A., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Idol, J. R., Karlins, E., Latic, P., Lee, J.-H., S.-Q., Lejaszki, R., Maduro, Q. L., Maduro, V. B., Marquies, E. H., Mastello, C., Maskeri, B., Mastrian, S. D., McCloskey, J. C., McDowell, J., Pajuelo, G. C., Pearson, R., Portnoy, M. R., Prasad, A., Schueler, M. C., Scantirip, S., Thomas, J. W., Thomas, P. J., Touchman, J. W., Tsaurian, C., Vogt, J. L., Walker, M. A., Wetherby, K. D., Wiggins, L., Young, A., Zhang, L. H. and Green, E. D.

REFERENCES
 2 (pages 1 to 174415)
 AUTHORS
 Green, E.D.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (24-APR-2002) NIH Intramural Sequencing Center, 8717

COMMENT ----- Genome Center
Government Circle, Gaithersburg, MD 20877, USA

Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: <http://www.nisc.nih.gov>
Contact: nisc_zoo@hghri.nih.gov
Project Information

```

-----Summary Statistics-----
Center project name: Q20
Center clone name: 309101

Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap, version 0.990319
Consensus quality: 172887 bases at least Q40
Consensus quality: 173032 bases at least Q30
Consensus quality: 173165 bases at least Q20
Insert size: 146000, agarose: fp
Insert size: 174119; sum-of-conligs
Quality coverage: 10.13x in Q20 bases; agarose-fp
Quality coverage: 8.50x in Q20 bases; sum-of-conligs

```

* NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

*	7424	confil of 7424 bp in length
*	7425	gap of unknown length
*	7525	confil of 4679 bp in length
*	51204	gap of unknown length
*	51304	confil of 52039 bp in length
*	103344	gap of unknown length
*	103345	confil of 70977 bp in length
*	103346	

FEATURES	LOCALION/QUALITY
SOURCE	1. 174419

misc_feature

```

/note="assembly_fragment
clone_end:SP6
vector_side:right"

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misc_feature

```
misc_feature      /note="assembly_fragment  
51304. 103342  
/note="assembly_fragment
```

misc_feature

	/note=assembly_fragment									
BASE COUNT	54243	a	33533	c	32461	g	53882	t	300	others
ORIGIN										

Query Match

38.08; Score 1089.2; DB 2; Length 174419;

Best Local Similarity: 92.58; Prod. No. 7.40 252;
Matches 178; Conservative 0; Mismatches 93; Indels 3;
Gaps 3

QY	1033	TTTTAAATTTTTTTTTTCTCCATATTTATTTATTTTAAATTTAACTTACATATTTATTT	1092
Db	50357	TTTTTCTTTTTTTTTTTTTTTTTTAACTTTATTTTTTAACTTTTAACTTTATTTATTT	50299
QY	1093	AGTTTCTGCAAAATATGCAAAATGAAATGCGGCGGCAAGATATGATGTTGCGCATCGGCAAC	1152
Db	50297	AGTTTTCTGCAAAATATGCAAAATGAAATGAAATGCAAGATATATGATGTTGCGCATCGGCAAC	50233
QY	1153	CGTCCGCGCGCGCGCGCGCGCGCGCATACGATCGCGCTGGCGCGCGCGCGCGCGCGCGCA	1211
Db	50237	CGTCCGCGCGCGCGCGCGCGCGCGCATACGATCGCGCTGGCGCGCGCGCGCGCGCGCGCA	5017
QY	1212	GATATGCAATATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT	1270
Db	50177	GATATGCAATATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT	5011
QY	1271	TGTTTCAATGATATGTTTCAATGATATGTTTCAATGATATGTTTCAATGATATGTTTCAAT	1330
Db	50117	TGTTTCAATGATATGTTTCAATGATATGTTTCAATGATATGTTTCAATGATATGTTTCAAT	5005
QY	1331	ACTGTTTCAATGATATGTTTCAATGATATGTTTCAATGATATGTTTCAATGATATGTTTCAAT	1390
Db	50057	ACTGTTTCAATGATATGTTTCAATGATATGTTTCAATGATATGTTTCAATGATATGTTTCAAT	4999
QY	1391	TTTTTAAATTTTAT	1450
Db	49997	TTTTTAAATTTTAT	4993
QY	1451	TGATCTGAT	1510
Db	49937	TGATCTGAT	4987
QY	1511	TTTTTAAATGCTGAT	1570
Db	49877	TTTTTAAATGCTGAT	4981
QY	1571	TCTGCTAT	1630
Db	49817	TCTGCTAT	4975
QY	1631	AACATTTGCTGAT	1690
Db	49757	AACATTTGCTGAT	4969
QY	1691	GGGCTTGGCTGAT	1750
Db	49697	GGGCTTGGCTGAT	4963
QY	1751	CTTATATGCTGAT	1810
Db	49637	CTTATATGCTGAT	4957
QY	1811	CTTATATGCTGAT	1870
Db	49577	CTTATATGCTGAT	4951
QY	1871	GTTGAATTTGCTGAT	1929
Db	49517	GTTGAATTTGCTGAT	4945
QY	1929	CTTATATGCTGAT	1989
Db	49457	CTTATATGCTGAT	4939
QY	1989	TCTTGGGCGCATTTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTTGG	2049
Db	49397	TCTTGGGCGCATTTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTTGG	4933
QY	2049	TTTATATTTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTT	2109
Db	49337	TTTATATTTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTTGGATTT	

[illegible]

```

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
COMMENT

Portnoy, M.E., Prasad, A., Scheller, M.G., Stanlidop, S., Thomas, J.W.,
Thomas, P.J., Touchman, R.W., Tsagaris, C., Voigt, L.L., Walker, M.A.,
Wetherby, K.D., Wiggins, B., Young, A.C., Zhang, H.-H. and Green, E.D.
NISC Comparative Sequencing Initiative
Unpublished
2 (bases 1 to 190078)
Green, E.D.
Direct Submission
Submitted (01-FPM-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 190078)
Genome Center
Submitted (U2-A95-2002) NIH Intramural Sequencing Center, #217
GroveMont Circle, Gaithersburg, MD 20877, USA
Oct Aug 2, 2002 This sequence version replaced gi|18464071.

Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc.zoohq@nsl.nih.gov
----- Project Information -----
Center project name: axn
Center clone name: 088B14

The sequence data in this record represents an "enhanced"
version of a Phase 2 submission. Specifically, the indicated
order and orientation of each sequence contig has been
established using one or more of the following: read-pair
data from individual subclones, overlaps with neighboring
clones, alignment with available reference sequence (e.g.,
human), and/or confirmation by PCR testing. In addition,
the sequence assembly is based on at least 8X average
coverage in G20 bases and has been reviewed to rule out
gross misassemblies; the low-quality ends of sequence
contigs have been trimmed away, and each base is associated
with a Phrap derived quality score.

Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye, 100% of reads
Assembly program: Phrap, Version 0.950319
Consensus quality: 18089 bases at least Q40
Consensus quality: 18985 bases at least Q30
Consensus quality: 18746 bases at least Q20
Insert size: 133000; agarose-fp
Insert size: 189478, sum of contigs
Quality coverage: 11.72x in Q20 bases; agarose-fp
Quality coverage: 8.23x in Q20 bases, sum of contigs

NOTE: This is a "working draft" sequence. It currently
consists of 7 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submitter.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
1
7697 contig of 7696 bp in length
7697 7796: gap of unknown length
14552 14751: gap of 8855 bp in length
14752 26766: contig of 12015 bp in length
26767 26867: gap of unknown length
31715 31814: gap of unknown length
31815 35938: contig of 4124 bp in length
35939 35938: gap of unknown length
35939 35938: contig of 5919 bp in length
35939 35938: gap of unknown length
35939 190078: contig of 34749 bp in length.

Location/Qualifiers
1..190078

```


130° TO 140°
S.L. 94/87

[illegible]

[illegible]

```

RESULT 15
AC109794
LOCUS
DEFINITION
AC109794
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
AC109794 166277 bp DNA linear HTG 07-FEB-2002
Species: Chone p42-44is, WOPRINO NIAFT SEQUENCE, 2 unordered
pieces.
AC109794 GI:18582004
HTG: HTGS_PHASPI; HTGS_DRAFT.
Bos laurus.
Bos laurus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Cetartiodactyla; Primantia; Pecora; Hovoidae;
Hovidae; Bovinae; Bos.
1 (bases 1 to 166277)
Akhtar, N., Ayele, K., Beckstrom-Sternberg, S. M., Benjamin, B.,
Blakesley, R. W., Bouliard, G. G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N. L., Granite, S., Guan, X., Gupta, J., Hashighi, P.,
Ho, S.-L., Idol, J. R., Karlins, E., Latic, P., Lee-Hin, S.-O.,
Legaspi, R., Maduro, G. L., Maduro, V. B., Mastello, C., Masker, H.,
Mastrian, S. D., McCloskey, J. C., McDowell, J., Pearson, R., Prasad, A.,
Shanilal, S., Thomas, D. M., Thomas, P. J., Touchman, J. W.,
Tsunobuchi, C., Vogt, J. L., Walker, M. A., Welteby, K. D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E. D.
NISC Comparative Sequencing Initiative
Unpublished
2 (bases 1 to 166277)
Green, E. D.
Direct Submission
Submitted (07-FEB-2002) NIH Intramural Sequencing Center, 8717
Grovecrest Circle, Gaithersburg, MD 20877, USA
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov

```

Contact: nisc_mouse@nhgri.nih.gov

Center project name: cjh
Center clone name: 499J06

Sequencing vector: plasmid, n/a; 100% of reads
chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap version 0.99.010

Consensus quality:	166045	bases at	least	Q40
Consensus quality:	166067	bases at	least	Q30
Consensus quality:	166073	bases at	least	Q30

Insert size: 145000; agarose-IP
Insert size: 146177; surf-ol contigs
Quality coverage: 12.63x in 910 bases; agarose-IP

Quality coverage: 12.69x in Q20 bases; agarose-lp
quality coverage: 10.92x in Q20 bases; sum of contigs

THE: This is a 'working draft' sequence. It currently consists of 2 configs. The true order of the pieces and how and what they do is not in the sequence record is

ditionally, gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence

1 51716: contig of 51716 bp in length
preserved.

51817 166277: count of 114461 bp in length
location/Qualifiers

/organism="Bos taurus"
/db_xref="taxon:9913"

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1..51716
/contig="assembly: fragment"
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clone_end: 17
vector_side: right
51817 166277
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/ note - assembly fragment
clone_end:SP6
vector_side:right"

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[illegible]

Similarity	89.68;	Pred. NO.	1.20	244;
Conservative	0;	Mismatches	133;	Indels
				3;
				Gaps
				3

ATGTTGGGATCCCAATGGGACTAATGTTTAAATTCTTTCCTCCAT 1058
- ||| -||- ||| -||| -||| -|||
-||| -||| -||| -||| -|||
-||| -||| -||| -||| -|||
-||| -||| -||| -||| -|||

TTATTTTAACTTACATAATTCATAGCTTTGGCAATATGCAAAATGCAATC 1118

GGGATACCATGTGTTGGCAAGCCCTCGCTGGCTTCTTCCTTCCCCAATACC 1178
TAAATTGAACCTTACCAATAATTAATAGATTGGCAGATATGGAAATGAAT 96393

AGGATACCTGAGTCCCATCCGAAACCTCCGCCCTCTCCCTCCCATACC 96453

CTATGCGTGGAGTGTAATTACCCCTCAAGCATTCAGATACTGTGCATGCCACTTC 96513

CAACTCG-TTCTACATGATTTTCCACATGTTTCATTGGCATTCCTCCAAATCT 1296

CTTCTCCCTCTCCACAGAGTCCAATAGACTGTTCTATACAATCAGTGCTCTTT 1356

TGGTAATGAGGATTAATGAAACATTTTAAATGGATATATATGCTTAA 1416
 CCCTCCTGCTCTCCAAAGAGACCCGAAGACAGATTAATACAAAGAGGACGCTTT 36634

